

#49



SEQUENCE LISTING

<110> Roberts, Shannon
Sherman, Amir
Trueheart, Joshua
Milne, G. Todd

<120> LOVE VARIANT REGULATOR MOLECULES

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<141> 2001-10-09

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 <400> 10
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<210> 36

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cacacagatc tcgtggccaa tttcttctag tttga

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cacacggatc cacaatgtta cgtcctgtag aaacccc

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<210> 38

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<400> 38

cacagcggcc gcttcattgt ttgcctccct gctg

34

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<211> 34

<212> DNA

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<223> primer

<400> 39

gcggccgcgg cgcccgccc atgtcaacaa gaat

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<223> primer

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Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
35 40 45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
50 55 60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65 70 75 80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
85 90 95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
100 105 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115 120 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
130 135 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145 150 155 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
165 170 175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
180 185 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195 200 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
210 215 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225 230 235 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys Arg Gln Gly Thr
245 250 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260 265 270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
275 280 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
290 295 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305 310 315 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325 330 335
Gly Glu Leu Phe Pro Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340 345 350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu

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      355              360              365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
  370              375              380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385              390              395              400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
      405              410              415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
      420              425              430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
      435              440              445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
  450              455              460
Asn Asn Ile Pro Pro
465

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<210> 42

<211> 469

<212> PRT

<213> Artificial Sequence

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<223> synthetically generated variant

<400> 42

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Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
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      20              25              30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
      35              40              45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
      50              55              60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65              70              75              80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
      85              90              95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
      100              105              110
Glu Ser His Ser Ser Asn Thr Ser Trp Gln Phe Leu Asp Pro Pro Asp
      115              120              125
Ser Tyr Asp Trp Leu Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
      130              135              140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145              150              155              160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
      165              170              175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
      180              185              190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
      195              200              205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210              215              220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225              230              235              240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
      245              250              255

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Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Gly Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
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<210> 43

<211> 469

<212> PRT

<213> Artificial Sequence

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<223> synthetically generated variant

<400> 43

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
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 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Val Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Ile Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln

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145          150          155          160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
          165          170          175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
          180          185          190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
          195          200          205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
          210          215          220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225          230          235          240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
          245          250          255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
          260          265          270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
          275          280          285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
          290          295          300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305          310          315          320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
          325          330          335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
          340          345          350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
          355          360          365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
          370          375          380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385          390          395          400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
          405          410          415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
          420          425          430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
          435          440          445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
          450          455          460
Asn Asn Ile Pro Pro
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<210> 44

<211> 469

<212> PRT

<213> Artificial Sequence

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<223> synthetically generated variant

<400> 44

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          20          25          30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
          35          40          45

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Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Gly Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
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<210> 45

<211> 469

<212> PRT

<213> Artificial Sequence

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<223> synthetically generated variant

<400> 45

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20          25          30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
35          40          45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
50          55          60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65          70          75          80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
85          90          95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
100         105         110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115         120         125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
130         135         140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145         150         155         160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
165         170         175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
180         185         190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195         200         205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
210         215         220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225         230         235         240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
245         250         255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260         265         270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
275         280         285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
290         295         300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305         310         315         320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325         330         335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340         345         350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
355         360         365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
370         375         380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385         390         395         400

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Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
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<210> 46

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<400> 46

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 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Tyr Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Lys Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Ala Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly

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      290              295              300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305              310              315              320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
      325              330              335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
      340              345              350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
      355              360              365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
      370              375              380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385              390              395              400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
      405              410              415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
      420              425              430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
      435              440              445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
      450              455              460
Asn Asn Ile Pro Pro
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<210> 47

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<212> PRT

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<400> 47

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Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1              5              10              15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
      20              25              30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
      35              40              45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
      50              55              60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
65              70              75              80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
      85              90              95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
      100             105             110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
      115             120             125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
      130             135             140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145             150             155             160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
      165             170             175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
      180             185             190

```


Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Ser Ile Pro Pro
 465

<210> 48

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 48

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| Met | Ser | Ser | Pro | Pro | Val | Pro | Ser | Gln | Ser | Leu | Pro | Leu | Asp | Val | Ser | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Glu | Ser | His | Ser | Ser | Asn | Thr | Ser | Arg | Gln | Phe | Leu | Asp | Pro | Pro | Asp | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Ser | Tyr | Asp | Trp | Ser | Trp | Thr | Ser | Ile | Gly | Thr | Asp | Glu | Ala | Ile | Asp | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Thr | Asp | Cys | Trp | Gly | Leu | Ser | Gln | Cys | Asp | Gly | Gly | Phe | Ser | Cys | Gln | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Leu | Glu | Pro | Thr | Leu | Pro | Asp | Leu | Pro | Ser | Pro | Phe | Glu | Ser | Thr | Val | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| Glu | Lys | Ala | Pro | Leu | Pro | Pro | Val | Ser | Ser | Asp | Ile | Ala | Arg | Ala | Ala | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| Ser | Ala | Gln | Arg | Glu | Leu | Phe | Asp | Asp | Leu | Ser | Ala | Val | Ser | Gln | Glu | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| Leu | Glu | Glu | Ile | Leu | Leu | Ala | Val | Thr | Val | Glu | Trp | Pro | Lys | Gln | Glu | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Ile | Trp | Thr | His | Pro | Ile | Gly | Met | Phe | Phe | Asn | Ala | Ser | Arg | Arg | Leu | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Leu | Thr | Val | Leu | Arg | Gln | Gln | Ala | Gln | Ala | Asp | Cys | His | Gln | Gly | Ala | | |
| | | | | 245 | | | | | | 250 | | | | 255 | | | |
| Leu | Asp | Glu | Cys | Leu | Arg | Thr | Lys | Asn | Leu | Phe | Thr | Ala | Val | His | Cys | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| Tyr | Ile | Leu | Asn | Val | Arg | Ile | Leu | Thr | Ala | Ile | Ser | Glu | Leu | Leu | Leu | | |
| | 275 | | | | | | 280 | | | | | 285 | | | | | |
| Ser | Gln | Ile | Arg | Arg | Thr | Gln | Asn | Ser | His | Met | Ser | Pro | Leu | Glu | Gly | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| Ser | Arg | Ser | Gln | Ser | Pro | Ser | Arg | Asp | Asp | Thr | Ser | Ser | Ser | Ser | Gly | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| His | Ser | Ser | Val | Asp | Thr | Ile | Pro | Phe | Phe | Ser | Glu | Asn | Leu | Pro | Ile | | |
| | | | | 325 | | | | | | 330 | | | | 335 | | | |
| Gly | Glu | Leu | Phe | Ser | Tyr | Val | Asp | Pro | Leu | Thr | His | Ala | Leu | Phe | Ser | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| Ala | Cys | Thr | Thr | Leu | His | Val | Gly | Val | Gln | Leu | Leu | Arg | Glu | Asn | Glu | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| Ile | Thr | Leu | Gly | Val | His | Ser | Ala | Gln | Gly | Ile | Ala | Ala | Ser | Ile | Ser | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| Met | Ser | Gly | Glu | Pro | Gly | Glu | Asp | Ile | Ala | Arg | Thr | Gly | Ala | Thr | Asn | | |
| 385 | | | | | 390 | | | | | 395 | | | | 400 | | | |
| Ser | Ala | Arg | Cys | Glu | Glu | Gln | Pro | Thr | Thr | Pro | Ala | Ala | Arg | Val | Leu | | |
| | | | | 405 | | | | | | 410 | | | | 415 | | | |
| Phe | Met | Phe | Leu | Ser | Asp | Glu | Gly | Ala | Phe | Gln | Glu | Ala | Lys | Ser | Ala | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Gly | Ser | Arg | Gly | Arg | Thr | Ile | Ala | Ala | Leu | Arg | Arg | Cys | Tyr | Glu | Asp | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| Ile | Phe | Ser | Leu | Ala | Arg | Lys | His | Lys | His | Gly | Met | Leu | Arg | Asp | Leu | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | |
| Asn | Ser | Ile | Pro | Pro | | | | | | | | | | | | | |
| 465 | | | | | | | | | | | | | | | | | |

<210> 49

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 49

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Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1          5          10          15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20          25          30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35          40          45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50          55          60
Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65          70          75          80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85          90          95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
100          105          110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115          120          125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
130          135          140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145          150          155          160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
165          170          175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
180          185          190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195          200          205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
210          215          220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225          230          235          240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
245          250          255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260          265          270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
275          280          285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
290          295          300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305          310          315          320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325          330          335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340          345          350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
355          360          365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
370          375          380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385          390          395          400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
405          410          415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
420          425          430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp

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435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Ser Ile Pro Pro
 465

<210> 50
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 50
 Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Arg Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Ala
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335

Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Ser Ile Pro Pro
 465

<210> 51
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 51
 Met Ala Ala Asp Gln Gly Ile Phe Met Asn Ser Val Thr Leu Ser Ala
 1 5 10 15
 Val Glu Gly Ser Arg Thr Ser Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Lys Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu

```

225          230          235          240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
          245          250          255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
          260          265          270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
          275          280          285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
          290          295          300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305          310          315          320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
          325          330          335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
          340          345          350
Ala Cys Thr Thr Leu His Val Gly Val Glu Leu Leu Arg Glu Asn Glu
          355          360          365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
          370          375          380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385          390          395          400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
          405          410          415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
          420          425          430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
          435          440          445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
          450          455          460
Asn Asn Ile Pro Pro
465

```

<210> 52

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 52

```

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
1          5          10          15
Val Glu Gly Ser His Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
          20          25          30
Arg Ala Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
          35          40          45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
          50          55          60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg His
65          70          75          80
Ser Arg Ala Ser Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
          85          90          95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
          100          105          110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
          115          120          125

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```

Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
130                      135                      140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                      150                      155                      160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                      165                      170                      175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
                      180                      185                      190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195                      200                      205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
210                      215                      220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                      230                      235                      240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                      245                      250                      255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260                      265                      270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
275                      280                      285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Asp Gly
290                      295                      300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305                      310                      315                      320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                      325                      330                      335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340                      345                      350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
355                      360                      365
Ile Thr Leu Gly Val Asp Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
370                      375                      380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                      390                      395                      400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
405                      410                      415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
420                      425                      430
Gly Ser Arg Gly Arg Thr Ile Thr Val Leu Arg Arg Ser Tyr Glu Asp
435                      440                      445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
450                      455                      460
Asn Asn Ile Pro Ser
465

```

<210> 53

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 53

```

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
1                      5                      10                      15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Ser | Cys | Asp | Arg | Cys | His | Ala | Gln | Lys | Ile | Lys | Cys | Thr | Gly | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Glu | Val | Thr | Gly | Arg | Ala | Pro | Cys | Gln | Arg | Cys | Gln | Gln | Ala | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Arg | Cys | Val | Tyr | Ser | Glu | Arg | Cys | Pro | Lys | Arg | Lys | Leu | Arg | Gln |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Arg | Ala | Ala | Asp | Leu | Val | Ser | Ala | Asp | Pro | Asp | Pro | Cys | Leu | His |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Met | Ser | Ser | Pro | Pro | Val | Pro | Ser | Gln | Ser | Leu | Pro | Leu | Asp | Val | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Ser | His | Ser | Ser | Asn | Thr | Ser | Arg | Gln | Phe | Leu | Asp | Pro | Pro | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Tyr | Asp | Trp | Ser | Trp | Thr | Ser | Ile | Gly | Thr | Asp | Glu | Ala | Ile | Asp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Thr | Asp | Cys | Trp | Gly | Leu | Ser | Gln | Cys | Asp | Gly | Gly | Phe | Ser | Cys | Gln |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Glu | Pro | Thr | Leu | Pro | Asp | Leu | Pro | Ser | Pro | Phe | Glu | Ser | Thr | Val |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Glu | Lys | Ala | Pro | Leu | Pro | Pro | Val | Ser | Ser | Asp | Ile | Ala | Arg | Ala | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ser | Ala | Gln | Arg | Glu | Leu | Phe | Asp | Asp | Leu | Ser | Ala | Val | Ser | Gln | Glu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Leu | Glu | Glu | Ile | Leu | Leu | Ala | Val | Thr | Val | Glu | Trp | Pro | Lys | Gln | Glu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ile | Trp | Thr | His | Pro | Ile | Gly | Met | Phe | Phe | Asn | Ala | Ser | Arg | Arg | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Thr | Val | Leu | Arg | Gln | Gln | Ala | Gln | Ala | Asp | Cys | His | Gln | Gly | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Leu | Asp | Glu | Cys | Leu | Arg | Thr | Lys | Asn | Leu | Phe | Thr | Ala | Val | His | Cys |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Tyr | Ile | Leu | Asn | Val | Arg | Ile | Leu | Thr | Ala | Ile | Ser | Glu | Leu | Leu | Leu |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Ser | Gln | Ile | Arg | Arg | Thr | Gln | Asn | Ser | His | Met | Ser | Pro | Leu | Glu | Gly |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ser | Arg | Ser | Gln | Ser | Pro | Ser | Arg | Asp | Asp | Thr | Ser | Ser | Ser | Ser | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| His | Ser | Ser | Val | Asp | Thr | Ile | Pro | Phe | Phe | Ser | Glu | Asn | Leu | Pro | Ile |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Gly | Glu | Leu | Phe | Ser | Tyr | Val | Asp | Pro | Leu | Thr | His | Ala | Leu | Phe | Ser |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ala | Cys | Thr | Thr | Leu | His | Val | Gly | Val | Gln | Leu | Leu | Arg | Glu | Asn | Glu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Ile | Thr | Leu | Gly | Val | His | Ser | Ala | Gln | Gly | Ile | Ala | Ala | Ser | Ile | Ser |
| | 370 | | | | | 375 | | | | | | | | | |

<210> 54
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated variant

<400> 54
 Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Ile Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
 100 105 110
 Asp Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asn Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Ser Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
 305 310 315 320
 His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
 325 330 335
 Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
 340 345 350
 Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Ile Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser

| | | | | |
|---|-----|-----|-----|-----|
| 370 | | 375 | | 380 |
| Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn | | | | |
| 385 | | 390 | | 400 |
| Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu | | | | |
| | 405 | | 410 | 415 |
| Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala | | | | |
| | 420 | | 425 | 430 |
| Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp | | | | |
| | 435 | | 440 | 445 |
| Ile Phe Ser Leu Ala Arg Lys His Lys Tyr Gly Met Leu Arg Asp Leu | | | | |
| | 450 | | 455 | 460 |
| Asn Asn Ile Pro Pro | | | | |
| 465 | | | | |

<210> 55

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 55

| | | | | |
|---|-----|--|-----|-----|
| Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro | | | | |
| 1 | 5 | | 10 | 15 |
| Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg | | | | |
| | 20 | | 25 | 30 |
| Arg Ser Cys Asp Arg Cys His Ala Gln Lys Val Lys Cys Thr Gly Asn | | | | |
| | 35 | | 40 | 45 |
| Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly | | | | |
| | 50 | | 55 | 60 |
| Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln | | | | |
| | 65 | | 70 | 75 |
| Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His | | | | |
| | 85 | | 90 | 95 |
| Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser | | | | |
| | 100 | | 105 | 110 |
| Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp | | | | |
| | 115 | | 120 | 125 |
| Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp | | | | |
| | 130 | | 135 | 140 |
| Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Phe Ser Cys Gln | | | | |
| | 145 | | 150 | 155 |
| Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val | | | | |
| | 165 | | 170 | 175 |
| Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala | | | | |
| | 180 | | 185 | 190 |
| Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu | | | | |
| | 195 | | 200 | 205 |
| Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu | | | | |
| | 210 | | 215 | 220 |
| Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu | | | | |
| | 225 | | 230 | 235 |
| Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr | | | | |
| | 245 | | 250 | 255 |
| Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys | | | | |
| | 260 | | 265 | 270 |

```

Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
    275                280                285
Ser Gln Ile Arg Arg Thr Leu Asn Ser His Met Ser Pro Leu Glu Gly
    290                295                300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
    305                310                315                320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
    325                330                335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
    340                345                350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
    355                360                365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
    370                375                380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
    385                390                395                400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
    405                410                415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
    420                425                430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
    435                440                445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
    450                455                460
Asn Asn Ile Pro Pro Cys
    465                470

```

<210> 56

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 56

```

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
  1                5                10                15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
    20                25                30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
    35                40                45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
    50                55                60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
    65                70                75                80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
    85                90                95
Met Ser Ser Pro Ser Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
    100                105                110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
    115                120                125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
    130                135                140
Thr Asp Cys Trp Gly Leu Ser Gln Arg Asp Gly Gly Phe Ser Ser Gln
    145                150                155                160
Leu Lys Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val

```

```
<210> 57
<211> 469
<212> PRT
<213> Artificial Sequence
```

| | | | | | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 57 | | | | | | | | | | | | | | | |
| Met | Ala | Ala | Asp | Gln | Gly | Ile | Phe | Thr | Asn | Ser | Val | Thr | Ile | Ser | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Val | Gly | Ser | Arg | Thr | Gly | Gly | Thr | Leu | Pro | Arg | Arg | Ala | Phe | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Ser | Cys | Asp | Arg | Cys | His | Ala | Gln | Lys | Ile | Lys | Cys | Thr | Gly | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Glu | Val | Thr | Gly | Arg | Ala | Pro | Cys | Gln | Arg | Cys | Gln | Gln | Ala | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |

```

Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65      70      75      80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
      85      90      95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
      100      105      110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
      115      120      125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Cys Thr Asp Glu Ala Ile Asp
      130      135      140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
      145      150      155      160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
      165      170      175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
      180      185      190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
      195      200      205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
      210      215      220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
      225      230      235      240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
      245      250      255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
      260      265      270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
      275      280      285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
      290      295      300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
      305      310      315      320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
      325      330      335
Gly Gly Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
      340      345      350
Ala Cys Thr Thr Leu His Val Gly Leu Gln Leu Leu Arg Glu Asn Glu
      355      360      365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
      370      375      380
Met Ser Gly Glu Ser Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Ser
      385      390      395      400
Ser Ala Arg Cys Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
      405      410      415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
      420      425      430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
      435      440      445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
      450      455      460
Asn Asn Ile Pro Pro
465

```

<210> 58

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 58

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Asp | Gln | Gly | Ile | Phe | Thr | Asn | Ser | Val | Thr | Leu | Ser | Pro | 1 | 5 | 10 | 15 |
| Val | Glu | Gly | Ser | Arg | Thr | Gly | Gly | Thr | Leu | Pro | Arg | Arg | Ala | Phe | Arg | 20 | 25 | 30 | |
| Arg | Ser | Cys | Asp | Arg | Cys | His | Ala | Arg | Lys | Ile | Lys | Cys | Thr | Gly | Asn | 35 | 40 | 45 | |
| Lys | Glu | Val | Thr | Gly | Arg | Ala | Pro | Cys | Gln | Arg | Cys | Gln | Gln | Ala | Gly | 50 | 55 | 60 | |
| Leu | Arg | Cys | Val | Tyr | Ser | Glu | Arg | Cys | Pro | Lys | Arg | Lys | Leu | Arg | Gln | 65 | 70 | 75 | 80 |
| Ser | Arg | Ala | Ala | Asp | Leu | Val | Ser | Ala | Asp | Pro | Asp | Pro | Cys | Leu | His | 85 | 90 | 95 | |
| Met | Ser | Ser | Pro | Pro | Val | Pro | Ser | Gln | Ser | Leu | Pro | Leu | Asp | Val | Ser | 100 | 105 | 110 | |
| Glu | Ser | His | Ser | Ser | Asn | Thr | Ser | Arg | Gln | Phe | Leu | Asp | Pro | Pro | Asp | 115 | 120 | 125 | |
| Ser | Tyr | Asp | Trp | Ser | Trp | Thr | Ser | Ile | Gly | Thr | Asp | Glu | Ala | Ile | Asp | 130 | 135 | 140 | |
| Thr | Asp | Cys | Trp | Gly | Leu | Ser | Gln | Cys | Asp | Gly | Gly | Phe | Ser | Cys | Gln | 145 | 150 | 155 | 160 |
| Leu | Glu | Pro | Thr | Leu | Pro | Asp | Leu | Pro | Ser | Pro | Phe | Glu | Tyr | Thr | Val | 165 | 170 | 175 | |
| Glu | Lys | Ala | Pro | Leu | Pro | Pro | Val | Ser | Ser | Asp | Ile | Ala | Arg | Ala | Ala | 180 | 185 | 190 | |
| Ser | Ala | Gln | Arg | Glu | Leu | Phe | Asp | Asp | Leu | Ser | Ala | Val | Ser | Gln | Glu | 195 | 200 | 205 | |
| Leu | Glu | Glu | Ile | Leu | Leu | Ala | Val | Thr | Val | Glu | Trp | Pro | Lys | Gln | Glu | 210 | 215 | 220 | |
| Ile | Trp | Thr | His | Pro | Ile | Gly | Met | Phe | Phe | Asn | Ala | Ser | Arg | Arg | Leu | 225 | 230 | 235 | 240 |
| Leu | Thr | Val | Leu | Arg | Gln | Gln | Ala | Gln | Ala | Asp | Cys | His | Gln | Gly | Thr | 245 | 250 | 255 | |
| Leu | Asp | Glu | Cys | Leu | Arg | Thr | Lys | Asn | Leu | Phe | Thr | Ala | Val | His | Cys | 260 | 265 | 270 | |
| Tyr | Ile | Leu | Asn | Val | Arg | Ile | Leu | Thr | Ala | Ile | Ser | Glu | Leu | Leu | Leu | 275 | 280 | 285 | |
| Ser | Gln | Ile | Arg | Arg | Thr | Gln | Asn | Ser | His | Met | Ser | Pro | Leu | Glu | Gly | 290 | 295 | 300 | |
| Ser | Arg | Ser | Gln | Ser | Pro | Ser | Arg | Asp | Asp | Thr | Ser | Ser | Ser | Ser | Gly | 305 | 310 | 315 | 320 |
| His | Ser | Ser | Val | Asp | Thr | Ile | Pro | Phe | Phe | Ser | Glu | Asn | Leu | Pro | Ile | 325 | 330 | 335 | |
| Gly | Glu | Leu | Phe | Ser | Tyr | Val | Asp | Pro | Leu | Thr | His | Ala | Leu | Phe | Ser | 340 | 345 | 350 | |
| Ala | Cys | Thr | Thr | Leu | His | Val | Gly | Val | Gln | Leu | Leu | Arg | Glu | Asn | Glu | 355 | 360 | 365 | |
| Ile | Thr | Leu | Gly | Val | His | Ser | Ala | Gln | Gly | Ile | Ala | Ala | Ser | Ile | Ser | 370 | 375 | 380 | |
| Met | Ser | Gly | Glu | Pro | Gly | Glu | Asp | Ile | Ala | Arg | Thr | Gly | Ala | Thr | Asn | 385 | 390 | 395 | 400 |
| Ser | Thr | Arg | Cys | Glu | Glu | Gln | Pro | Thr | Thr | Pro | Ala | Ala | Arg | Val | Leu | 405 | 410 | 415 | |

Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
 465

<210> 59

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 59

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Leu Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Ile Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Gln Val Pro Ser Gln Ser Leu Ser Leu Asp Ile Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
 245 250 255
 Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
 260 265 270
 Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
 275 280 285
 Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
 290 295 300
 Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly

```

305          310          315          320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
          325          330          335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
          340          345          350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
          355          360          365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
          370          375          380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385          390          395          400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
          405          410          415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
          420          425          430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
          435          440          445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
          450          455          460
Asn Asn Ile Pro Pro
465

```

<210> 60

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 60

```

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1          5          10          15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
          20          25          30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
          35          40          45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
          50          55          60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65          70          75          80
Ser Arg Ala Ala Asn Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
          85          90          95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser
          100          105          110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
          115          120          125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Glu Ala Phe Asp
          130          135          140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145          150          155          160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
          165          170          175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
          180          185          190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
          195          200          205

```



```

Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210                      215                220
Ile Trp Thr His Pro Ile Gly Ile Phe Phe Asn Ala Ser Arg Arg Leu
225                      230                235                240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                      245                250                255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
                      260                265                270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
                      275                280                285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
                      290                295                300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Ile Ser Ser Ser Ser Gly
305                      310                315                320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                      325                330                335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
                      340                345                350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
                      355                360                365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Tyr Ile Ser
                      370                375                380
Lys Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                      390                395                400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                      405                410                415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
                      420                425                430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
                      435                440                445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
                      450                455                460
Asn Asn Ile Pro Pro
465

```

<210> 61

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 61

```

Met Ala Ala Asp Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1                      5                      10                15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
                      20                      25                30
Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Ile Gly Asn
                      35                      40                45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Arg Ala Gly
50                      55                      60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Arg Leu Arg Gln
65                      70                      75                80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
                      85                      90                95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | 100 | | | | | 105 | | | | 110 | | | |
| Glu | Ser | His | Ser | Ser | Asn | Thr | Ser | Arg | Gln | Phe | Leu | Asp | Pro | Pro | Asp |
| | | 115 | | | | | | 120 | | | | 125 | | | |
| Ser | Tyr | Asp | Trp | Ser | Trp | Thr | Ser | Ile | Gly | Thr | Asp | Glu | Ala | Ile | Asp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Thr | Asp | Cys | Trp | Gly | Leu | Ser | Gln | Cys | Asp | Gly | Gly | Phe | Ser | Cys | Gln |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 |
| Leu | Glu | Pro | Thr | Leu | Pro | Asp | Leu | Pro | Ser | Pro | Phe | Glu | Ser | Thr | Val |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Glu | Lys | Ala | Pro | Leu | Pro | Pro | Val | Ser | Ser | Asp | Ile | Ala | Arg | Ala | Ala |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Ser | Ala | Gln | Arg | Glu | Leu | Phe | Asp | Asp | Leu | Ser | Ala | Val | Ser | Gln | Glu |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Leu | Glu | Glu | Ile | Leu | Leu | Ala | Val | Thr | Val | Glu | Trp | Pro | Lys | Gln | Glu |
| | 210 | | | | | 215 | | | | 220 | | | | | |
| Ile | Trp | Thr | His | Pro | Ile | Gly | Met | Phe | Phe | Asn | Ala | Ser | Arg | Arg | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Thr | Val | Leu | Arg | Gln | Gln | Ala | Gln | Ala | Asp | Cys | His | Gln | Gly | Thr |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Leu | Asp | Glu | Cys | Leu | Arg | Thr | Lys | Asn | Leu | Phe | Thr | Ala | Val | His | Cys |
| | | 260 | | | | | | 265 | | | | | 270 | | |
| Tyr | Ile | Leu | Asn | Val | Arg | Ile | Leu | Thr | Ala | Ile | Ser | Glu | Leu | Leu | Leu |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Ser | Gln | Ile | Arg | Arg | Thr | Gln | Asn | Ser | His | Met | Ser | Pro | Leu | Glu | Gly |
| | 290 | | | | 295 | | | | | | 300 | | | | |
| Ser | Arg | Ser | Gln | Ser | Pro | Ser | Arg | Asp | Asp | Thr | Ser | Ser | Ser | Ser | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| His | Ser | Cys | Val | Asp | Thr | Ile | Pro | Phe | Phe | Ser | Glu | Asn | Leu | Pro | Ile |
| | | | 325 | | | | | 330 | | | | | 335 | | |
| Gly | Glu | Leu | Phe | Ser | Tyr | Val | Asp | Pro | Leu | Thr | His | Ala | Leu | Phe | Ser |
| | | 340 | | | | | | 345 | | | | 350 | | | |
| Ala | Cys | Thr | Thr | Leu | His | Val | Gly | Val | Gln | Leu | Leu | Arg | Glu | Tyr | Glu |
| | 355 | | | | | | 360 | | | | | 365 | | | |
| Ile | Thr | Leu | Gly | Ile | His | Ser | Ala | Gln | Gly | Ile | Ala | Ala | Ser | Ile | Ser |
| | 370 | | | | | 375 | | | | 380 | | | | | |
| Met | Ser | Gly | Glu | Pro | Gly | Glu | Asp | Ile | Ala | Arg | Thr | Gly | Ala | Thr | Asn |
| 385 | | | | | 390 | | | | 395 | | | | | | 400 |
| Ser | Ala | Arg | Cys | Glu | Glu | Gln | Pro | Thr | Thr | Pro | Ala | Ala | Arg | Val | Leu |
| | | | 405 | | | | | 410 | | | | | 415 | | |
| Phe | Met | Phe | Leu | Ser | Asp | Glu | Gly | Ala | Phe | Gln | Glu | Ala | Lys | Ser | Ala |
| | | 420 | | | | | 425 | | | | | 430 | | | |
| Gly | Ser | Arg | Gly | Arg | Thr | Ile | Ala | Ala | Leu | Arg | Arg | Cys | Tyr | Glu | Asp |
| | 435 | | | | | 440 | | | | | 445 | | | | |
| Ile | Phe | Ser | Leu | Ala | Arg | Lys | His | Lys | His | Gly | Met | Leu | Arg | Asp | Leu |
| | 450 | | | | 455 | | | | | 460 | | | | | |
| Asn | Asn | Ile | Pro | Pro | | | | | | | | | | | |
| 465 | | | | | | | | | | | | | | | |

<210> 62

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 62

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|------------|------------|------------|------------|----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|-----|
| Met 1 | Ala | Ala | Asp | Gln 5 | Gly | Ile | Phe | Thr | Asn 10 | Ser | Val | Thr | Leu | Ser 15 | Pro |
| Val | Glu | Gly | Ser 20 | Arg | Thr | Gly | Gly | Thr 25 | Leu | Pro | Arg | Arg | Ala 30 | Phe | Arg |
| Arg | Ser | Cys 35 | Asp | Arg | Cys | His | Ala 40 | Arg | Lys | Ile | Lys | Cys 45 | Thr | Gly | Asn |
| Lys | Glu 50 | Val | Thr | Gly | Arg | Ala 55 | Pro | Cys | Gln | Arg | Cys 60 | Gln | Gln | Ala | Gly |
| Leu 65 | Arg | Cys | Val | Tyr | Ser 70 | Glu | Arg | Cys | Pro | Lys 75 | Arg | Lys | Leu | Arg | Gln |
| Ser | Arg | Ala | Ala 85 | Asp | Leu | Val | Ser | Ala 90 | Asp | Pro | Asp | Pro | Cys 95 | Leu | His |
| Met | Ser | Ser | Pro 100 | Pro | Val | Pro | Ser | Gln 105 | Ser | Leu | Pro | Leu | Asp 110 | Val | Ser |
| Glu | Ser | His 115 | Ser | Ser | Asn | Thr | Ser 120 | Arg | Gln | Phe | Leu | Asp 125 | Pro | Pro | Asp |
| Ser | Tyr 130 | Asp | Trp | Ser | Trp | Thr 135 | Ser | Ile | Gly | Thr | Asp 140 | Glu | Ala | Ile | Asp |
| Thr 145 | Asp | Cys | Trp | Gly | Leu 150 | Ser | Gln | Cys | Asp | Gly 155 | Gly | Phe | Ser | Cys | Gln |
| Leu | Glu | Pro | Thr 165 | Leu | Pro | Asp | Leu | Pro | Ser 170 | Pro | Phe | Glu | Ser | Thr | Val |
| Glu | Lys | Ala 180 | Pro | Leu | Pro | Pro | Val | Ser 185 | Ser | Asp | Ile | Ala | Arg 190 | Ala | Ala |
| Ser | Ala | Gln 195 | Arg | Glu | Leu | Phe | Asp 200 | Asp | Leu | Ser | Ala 205 | Val | Ser | Gln | Glu |
| Leu | Glu 210 | Glu | Ile | Leu | Leu | Ala 215 | Val | Thr | Val | Glu | Trp 220 | Pro | Lys | Gln | Glu |
| Ile 225 | Trp | Thr | His | Pro | Ile 230 | Gly | Met | Phe | Phe | Asn 235 | Ala | Ser | Arg | Arg | Leu |
| Leu | Thr | Val | Leu 245 | Arg | Gln | Gln | Ala | Gln | Ala 250 | Asp | Cys | His | Gln | Gly | Thr |
| Leu | Asp | Glu | Cys 260 | Leu | Arg | Thr | Lys | Asn 265 | Leu | Phe | Thr | Ala | Val 270 | His | Cys |
| Tyr | Ile 275 | Leu | Asn | Val | Arg | Ile | Leu 280 | Thr | Ala | Ile | Ser | Glu 285 | Leu | Leu | Leu |
| Ser | Gln 290 | Ile | Arg | Arg | Ile | Gln | Asn 295 | Ser | His | Met | Ser 300 | Pro | Leu | Glu | Gly |
| Ser 305 | Arg | Ser | Gln | Ser | Leu 310 | Ser | Arg | Asp | Asp | Thr 315 | Ser | Ser | Ser | Ser | Gly |
| His | Ser | Ser | Val 325 | Asp | Thr | Ile | Pro | Phe 330 | Phe | Ser | Glu | Asn | Leu 335 | Pro | Ile |
| Asp | Glu | Leu | Phe 340 | Ser | Tyr | Val | Asp 345 | Pro | Leu | Thr | His | Ala | Leu 350 | Phe | Ser |
| Ala | Cys | Thr 355 | Thr | Leu | His | Val | Gly 360 | Val | Gln | Leu | Leu | Arg 365 | Glu | Asn | Glu |
| Ile | Thr 370 | Leu | Gly | Val | His | Ser 375 | Ala | Gln | Gly | Ile | Ala 380 | Ala | Ser | Ile | Ser |
| Met 385 | Ser | Gly | Glu | Leu | Gly 390 | Glu | Asp | Ile | Val | Arg 395 | Thr | Gly | Ala | Thr | Asn |
| Ser | Ala | Arg | Cys 405 | Glu | Glu | Gln | Pro | Thr | Thr 410 | Pro | Ala | Ala | Arg 415 | Val | Leu |
| Phe | Met | Phe 420 | Leu | Ser | Asp | Glu | Gly | Ala 425 | Phe | Gln | Glu | Ala | Lys 430 | Ser | Ala |
| Gly | Ser | Arg 435 | Ser | Arg | Thr | Ile | Ala 440 | Ala | Leu | Arg | Arg | Cys 445 | Tyr | Glu | Asp |
| Ile | Phe | Ser | Leu | Ala | Arg | Lys | His | Lys | His | Gly | Met | Leu | Arg | Asp | Leu |

450
Asn Asn Ile Pro Pro
465

455

460

<210> 63
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated variant

<400> 63
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1 5 10 15
Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
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Arg Ser Cys Asp Arg Cys His Ala Gln Lys Ile Lys Cys Thr Gly Asn
35 40 45
Lys Glu Val Asn Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
50 55 60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
65 70 75 80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
85 90 95
Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Ile Ser
100 105 110
Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
115 120 125
Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Ile Asp Glu Ala Ile Asp
130 135 140
Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145 150 155 160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
165 170 175
Glu Lys Ala Pro Leu Pro Pro Ile Ser Ser Asp Ile Ala Arg Ala Ala
180 185 190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
195 200 205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
210 215 220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225 230 235 240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
245 250 255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
260 265 270
Tyr Ile Leu Asn Val Arg Ile Leu Ala Ala Ile Ser Glu Leu Leu Leu
275 280 285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
290 295 300
Ser Arg Ser Gln Ser Pro Ser Arg Asp Asp Thr Ser Ser Ser Ser Gly
305 310 315 320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
325 330 335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
340 345 350

Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
 355 360 365
 Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
 370 375 380
 Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
 385 390 395 400
 Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
 405 410 415
 Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Ala Lys Ser Ala
 420 425 430
 Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
 435 440 445
 Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
 450 455 460
 Asn Asn Ile Pro Pro
 465

<210> 64

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 64

Met Ala Ala Glu Gln Gly Ile Phe Thr Asn Ser Val Thr Leu Ser Pro
 1 5 10 15
 Val Glu Gly Ser Arg Thr Gly Gly Thr Leu Pro Arg Arg Ala Phe Arg
 20 25 30
 Arg Ser Cys Asp Arg Cys His Ala Arg Lys Ile Lys Cys Thr Gly Asn
 35 40 45
 Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50 55 60
 Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65 70 75 80
 Ser Arg Ala Ala Asp Leu Ile Ser Ala Asp Pro Asp Pro Cys Leu His
 85 90 95
 Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Glu Val Ser
 100 105 110
 Glu Ser His Ser Ser Asn Thr Ser Arg Gln Phe Leu Asp Pro Pro Asp
 115 120 125
 Ser Tyr Asp Trp Ser Trp Thr Ser Ile Gly Thr Asp Lys Ala Ile Asp
 130 135 140
 Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
 145 150 155 160
 Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
 165 170 175
 Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Thr Arg Ala Ala
 180 185 190
 Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
 195 200 205
 Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
 210 215 220
 Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
 225 230 235 240
 Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr


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Thr Asp Cys Trp Gly Leu Ser Gln Cys Asp Gly Gly Phe Ser Cys Gln
145                               150                               155                               160
Leu Glu Pro Thr Leu Pro Asp Leu Pro Ser Pro Phe Glu Ser Thr Val
                               165                               170                               175
Glu Lys Ala Pro Leu Pro Pro Val Ser Ser Asp Ile Ala Arg Ala Ala
                               180                               185                               190
Ser Ala Gln Arg Glu Leu Phe Asp Asp Leu Ser Ala Val Ser Gln Glu
                               195                               200                               205
Leu Glu Glu Ile Leu Leu Ala Val Thr Val Glu Trp Pro Lys Gln Glu
                               210                               215                               220
Ile Trp Thr His Pro Ile Gly Met Phe Phe Asn Ala Ser Arg Arg Leu
225                               230                               235                               240
Leu Thr Val Leu Arg Gln Gln Ala Gln Ala Asp Cys His Gln Gly Thr
                               245                               250                               255
Leu Asp Glu Cys Leu Arg Thr Lys Asn Leu Phe Thr Ala Val His Cys
                               260                               265                               270
Tyr Ile Leu Asn Val Arg Ile Leu Thr Ala Ile Ser Glu Leu Leu Leu
                               275                               280                               285
Ser Gln Ile Arg Arg Thr Gln Asn Ser His Met Ser Pro Leu Glu Gly
                               290                               295                               300
Ser Arg Ser Gln Ser Pro Ser Gly Asp Asp Thr Ser Ser Ser Ser Gly
305                               310                               315                               320
His Ser Ser Val Asp Thr Ile Pro Phe Phe Ser Glu Asn Leu Pro Ile
                               325                               330                               335
Gly Glu Leu Phe Ser Tyr Val Asp Pro Leu Thr His Ala Leu Phe Ser
                               340                               345                               350
Ala Cys Thr Thr Leu His Val Gly Val Gln Leu Leu Arg Glu Asn Glu
                               355                               360                               365
Ile Thr Leu Gly Val His Ser Ala Gln Gly Ile Ala Ala Ser Ile Ser
                               370                               375                               380
Met Ser Gly Glu Pro Gly Glu Asp Ile Ala Arg Thr Gly Ala Thr Asn
385                               390                               395                               400
Ser Ala Arg Cys Glu Glu Gln Pro Thr Thr Pro Ala Ala Arg Val Leu
                               405                               410                               415
Phe Met Phe Leu Ser Asp Glu Gly Ala Phe Gln Glu Gly Lys Ser Ala
                               420                               425                               430
Gly Ser Arg Gly Arg Thr Ile Ala Ala Leu Arg Arg Cys Tyr Glu Asp
                               435                               440                               445
Ile Phe Ser Leu Ala Arg Lys His Lys His Gly Met Leu Arg Asp Leu
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Asn Asn Ile Pro Pro
465

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<210> 66

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 66

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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300

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ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcagtttc ttgatccacc ggacagctac gactgggtcgt ggacctcgat tggcactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaaca agcgcaggcc gactgccgtc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga ccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcagaacc tccctattgg tgagctgttc 1020
ccctatgttg accccctgac acacgcccta ttctcggtt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgcca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgtctggt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

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<210> 67

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 67

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caaaagatca aatgtactgg aaataaggag gttactggcc gtgtccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgtgac ccagatccct gcttgacat gtccctcgct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
tggcaatttc ttgatccacc ggacagctac gactgggtgt ggacctcgat tggcactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagagtgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga ccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccc agcagagacg acaccagcag cagcagcggc 960
cacggcagtg ttgacaccat acccttcttt agcagaacc tccctattgg tgagctgttc 1020
tccatgttg accccctgac acacgcccta ttctcggtt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtac actccgcca gggcattgca 1140
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tccgcaagat gcgaggagca gccgaccact ccagcggctc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgtctggt cccgaggtcg aaccatcgca 1320
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ctcagagacc tcaacaatat tcctccatga 1410

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<210> 68

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 68

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caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggtag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgcct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctgt ggatctcgat tggcactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaac agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
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ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020
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agtgatgaag gggctttcca ggaggcaaag tctgtgtggt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

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<210> 69

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 69

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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgccaa 240
tccagggtag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgcct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctcgat tggcactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaac agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctattgg tgagctgttc 1020

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tctatgttg accccctgac acacgccta ttctcggtt gactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtag actccgcca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgaccact ccagcggtc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tctccatga 1410

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<210> 70

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 70

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caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggtatttg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggcctgac ggtagaatgg 660
ccgaagcagg aaatctggac ccattccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttaacgacca agaacctctt tacggcagta cactgttaca tattgaatgt gcgattttg 840
accgccatat cggagttgct cctgtcgcaa attaggcgga cccagaacag ccatatgagc 900
ccactggaag ggagtcgatc ccagtgcgcg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctatttg tgagctgttc 1020
tctatgttg accccctgac acacgccta ttctcggtt gactacgtt acatgttggg 1080
gtacaattgc tgcgtgagaa tgagattact ctgggagtag actccgcca gggcattgca 1140
gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcgaccaat 1200
tccgcaagat gcgaggagca gccgactact ccagcggtc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tctccatga 1410

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<210> 71

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 71

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cgcaccggtg gaacattacc ccgcctgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360

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```

<210> 72

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 72

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cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgcca 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
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cggcaatttc ttgatccacc ggacagctac gactgggtcgt ggacctcgat tggcactgac 420
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gacctgtcgg cgggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
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<210> 73

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 73

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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtccctgcct 300
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cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gtggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
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```

<210> 74

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 74

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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgacgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ttctgctgac ccagatccct gcttgacat gtccctgcct 300
ccagtgcctt cacagagctt gccactagac gtatccgagt cgcattcctc aaataacctc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
ttacggacca agaacctctt tacggcagta cactgttaca tattgaacgt gcggattttg 840
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ccactgaaag ggagtcgatc ccagtcgccg agcagagacg acaccagcag cagcagcggc 960
cacagcagtg ttgacaccat acccttcttt agcgagaacc tccctatttg tgagctgttc 1020
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```

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gtacaattgc tgcgtgagaa tgagattact ctgggagtag actccgcccc gggcattgca 1140
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tccgcaagat gcgaggagca gccgaccact ccagcggtc gggttttgtt catgttcttg 1260
agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 75

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 75

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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
aaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcggttg 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
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cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacgggttg aaaagctccg 540
ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
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cttactgtcc tgcgccaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 76

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 76

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cgcaccagtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
aaaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcggttg 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcactgac 420

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```

gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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ttgccaccgg tatcgagcga cattgctcgt ggggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
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ctcagagacc tcaacaatat tcctccatga 1410

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<210> 77

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 77

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cacaccggtg gaacattacc ccgcgctgca ttccgacgcg cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccat 240
tccagggcat cggatctcgt ctctgctgac ccagatccct gcttgacat gtccctcgct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctcg ggacctcgat tggcactgac 420
gaggctattg acactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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gacctgtcgg cgggtgtcgca ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
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gtactgcgac gaagctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tccttcatga 1410

```

<210> 78

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 78

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caaaagatca aatgtactgg aaataaggag gttactggcc gtgtccctg tcagcgttgc 180
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ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 79

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 79

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cgcaccggtg gaacattacc ccgccgtgca ctccgacgct cttgtgatcg gtgtcatgca 120
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tcctatgttg accccctgac acacgcccta ttctcggtt gcactacgtt acatgttggg 1080
gtacaattgc tgcgtgagat tgagattact ctgggagtag actccgcccc gggcattgca 1140

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gcttccatca gcatgagcgg ggaaccaggc gaggatatag ccaggacagg ggcaaccaat 1200
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agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggctg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa atatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 80

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 80

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cgcaccgggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagggtca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
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<210> 81

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 81

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caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gttacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
tcagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctgat tggcactgac 420
gaggtatttg aactgactg ctgggggctg tcccaacgtg atggaggctt cagctctcag 480

```



```

ttaaagccaa cgctgccgga tctaccttcg ccttcgagtg ctacgggtga aaaagctccg 540
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gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
cttactgtcc tgcgccaaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
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ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 82

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 82

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cgcaccgggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gaggcatgcc ccaagcgcaa gctacgcca 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
ccagtgcctt cacagagttt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctgat ttgactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 83

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 83

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cgaaagatca aatgtactgg aaataaggag gttactggcc gtgtccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
ccagtgccct cacagagctt gccgctagac gtatccgagt cgcattcctc aaataacctc 360
cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctgat tggcactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
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cttactgtcc tgcgccaaac agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 84

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 84

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cgcaccggtg gaacattacc ccgccgtgca ttgcgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttattggcc gtgtccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtatacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
caagtgccct cacagagctt gtgcgtagac atatccgagt cgcattcctc aaataacctc 360
cggcaatttc ttgatccacc ggacagctac gactggctgt ggacctgat tggcactgac 420
gaggctattg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
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ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcgtc acgacggctt 720
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```
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agtgatgaag gggcattcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcttccatga 1410
```

<210> 85

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 85

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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtacttg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgcaa 240
tccagggcag cgaatctcgt ctctgctgac ccagatccct gcttacacat gtcctcgct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctcg ggacctcgat tggcactgac 420
gaggtttttg aactgactg ctgggggcta tcccaatgtg atggaggctt cagctgtcag 480
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agtgatgaag gggctttcca ggaggcaaag tctgctggtt cccgaggtcg aaccatcgca 1320
gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcttccatga 1410
```

<210> 86

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 86

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cgcaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtatttg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
caacgggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcag gctacgcaa 240
tccagggcag cggatctcgt ctctgctgac ccagatccct gcttgacat gtcctcgct 300
ccagtgcctt cacagagctt gccgctagac gtatccgagt cgcattcctc aaatacctcc 360
cggcaatttc ttgatccacc ggacagctac gactggctcg ggacctcgat tggcactgac 420
gaggtatttg aactgactg ctgggggctg tcccaatgtg atggaggctt cagctgtcag 480
ttagagccaa cgctgccgga tctaccttcg cccttcgagt ctacggttga aaaagctccg 540
```

```

ttgccaccgg tatcgagcga cattgctcgt gcggccagtg cgcaacgaga gcttttcgat 600
gacctgtcgg cgggtgtcga ggaactggaa gagatccttc tggccgtgac ggtagaatgg 660
ccgaagcagg aaatctggac ccatcccatc ggaatgtttt tcaatgcttc acgacggctt 720
cttactgtcc tgcgccaaaca agctcaggcc gactgccatc aaggcacact agacgaatgt 780
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagatc tcaacaatat tcctccatga 1410

```

<210> 87

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 87

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cgcaaccggtg gaacattacc ccgccgtgca ttccgacgct cttgtgatcg gtgtcatgca 120
cgaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
cagcaagctg gacttcgatg cgtctatagt cagcgatgcc ccaagcgcaa gctacgcaa 240
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cttactgtcc tgcgccaaaca agcgcaggcc gactgccatc aaggcacact agacgaatgt 780
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ctcagagacc tcaacaatat tcctccatga 1410

```

<210> 88

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 88

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cgcaccggtg gaacattacc ccgcogtgca ttccgacgct cttgtgatcg gtgtcatgca 120
caaaagatca aatgtactgg aaataaggag gttaatggcc gtgctccctg tcagcgttgc 180
cagcaggctg gacttcgatg cgtctacagt gagcgatgcc ccaagcgcaa gctacgccaa 240
tccagggcag cggatctcgt ctctgttgac ccagatccct gcttgacat gtcctcgct 300
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cggcaatttc ttgatccacc ggacagctac gactggtcgt ggacctcgat tggcattgac 420
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ttgccaccga tatcgagcga cattgctcgt ggggccagtg cgcaacgaga gcttttcgat 600
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ttacggacca agaacctctt tacggcagta cactgttaca tattgaatgt gcggattttg 840
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gcactgcgac gatgctatga ggatatcttt tccctcgccc gcaaacacaa acatggcatg 1380
ctcagagacc tcaacaatat tcttccatga 1410

```

<210> 89

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated variant

<400> 89

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cgcaccggtg gaacattacc ccgcogtgca ttccgacgct cttgtgatcg gtgtcatgca 120
cgaaagatca aatgtactgg aaataaggag gttactggcc gtgctccctg tcagcgttgc 180
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<211> 1410

<212> DNA

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<220>

<223> synthetically generated variant

<400> 90

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<210> 91

<211> 469

<212> PRT

<213> *Aspergillus terreus*

<400> 91

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 35           40           45
Lys Glu Val Thr Gly Arg Ala Pro Cys Gln Arg Cys Gln Gln Ala Gly
 50           55           60
Leu Arg Cys Val Tyr Ser Glu Arg Cys Pro Lys Arg Lys Leu Arg Gln
 65           70           75           80
Ser Arg Ala Ala Asp Leu Val Ser Ala Asp Pro Asp Pro Cys Leu His
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Met Ser Ser Pro Pro Val Pro Ser Gln Ser Leu Pro Leu Asp Val Ser

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| | | | | | | | | | | | | | | | | | |
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| Ser | Tyr | Asp | Trp | Ser | Trp | Thr | Ser | Ile | Gly | Thr | Asp | Glu | Ala | Ile | Asp | | |
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| Thr | Asp | Cys | Trp | Gly | Leu | Ser | Gln | Cys | Asp | Gly | Gly | Phe | Ser | Cys | Gln | | |
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| Leu | Glu | Pro | Thr | Leu | Pro | Asp | Leu | Pro | Ser | Pro | Phe | Glu | Ser | Thr | Val | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | |
| Glu | Lys | Ala | Pro | Leu | Pro | Pro | Val | Ser | Ser | Asp | Ile | Ala | Arg | Ala | Ala | | |
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| Ser | Ala | Gln | Arg | Glu | Leu | Phe | Asp | Asp | Leu | Ser | Ala | Val | Ser | Gln | Glu | | |
| | 195 | | | | | | 200 | | | | | 205 | | | | | |
| Leu | Glu | Glu | Ile | Leu | Leu | Ala | Val | Thr | Val | Glu | Trp | Pro | Lys | Gln | Glu | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Ile | Trp | Thr | His | Pro | Ile | Gly | Met | Phe | Phe | Asn | Ala | Ser | Arg | Arg | Leu | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Leu | Thr | Val | Leu | Arg | Gln | Gln | Ala | Gln | Ala | Asp | Cys | His | Gln | Gly | Thr | | |
| | | | 245 | | | | | | 250 | | | | | 255 | | | |
| Leu | Asp | Glu | Cys | Leu | Arg | Thr | Lys | Asn | Leu | Phe | Thr | Ala | Val | His | Cys | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | |
| Tyr | Ile | Leu | Asn | Val | Arg | Ile | Leu | Thr | Ala | Ile | Ser | Glu | Leu | Leu | Leu | | |
| | 275 | | | | | | 280 | | | | | 285 | | | | | |
| Ser | Gln | Ile | Arg | Arg | Thr | Gln | Asn | Ser | His | Met | Ser | Pro | Leu | Glu | Gly | | |
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| Ser | Arg | Ser | Gln | Ser | Pro | Ser | Arg | Asp | Asp | Thr | Ser | Ser | Ser | Ser | Gly | | |
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| His | Ser | Ser | Val | Asp | Thr | Ile | Pro | Phe | Phe | Ser | Glu | Asn | Leu | Pro | Ile | | |
| | | | 325 | | | | | 330 | | | | | 335 | | | | |
| Gly | Glu | Leu | Phe | Ser | Tyr | Val | Asp | Pro | Leu | Thr | His | Ala | Leu | Phe | Ser | | |
| | | 340 | | | | | 345 | | | | | 350 | | | | | |
| Ala | Cys | Thr | Thr | Leu | His | Val | Gly | Val | Gln | Leu | Leu | Arg | Glu | Asn | Glu | | |
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| Ile | Thr | Leu | Gly | Val | His | Ser | Ala | Gln | Gly | Ile | Ala | Ala | Ser | Ile | Ser | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| Met | Ser | Gly | Glu | Pro | Gly | Glu | Asp | Ile | Ala | Arg | Thr | Gly | Ala | Thr | Asn | | |
| 385 | | | | 390 | | | | | 395 | | | | | | 400 | | |
| Ser | Ala | Arg | Cys | Glu | Glu | Gln | Pro | Thr | Thr | Pro | Ala | Ala | Arg | Val | Leu | | |
| | | | 405 | | | | | 410 | | | | | 415 | | | | |
| Phe | Met | Phe | Leu | Ser | Asp | Glu | Gly | Ala | Phe | Gln | Glu | Ala | Lys | Ser | Ala | | |
| | | 420 | | | | | 425 | | | | | 430 | | | | | |
| Gly | Ser | Arg | Gly | Arg | Thr | Ile | Ala | Ala | Leu | Arg | Arg | Cys | Tyr | Glu | Asp | | |
| | 435 | | | | | 440 | | | | | 445 | | | | | | |
| Ile | Phe | Ser | Leu | Ala | Arg | Lys | His | Lys | His | Gly | Met | Leu | Arg | Asp | Leu | | |
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<210> 92

<211> 1410

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<213> *Aspergillus terreus*

<400> 92

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